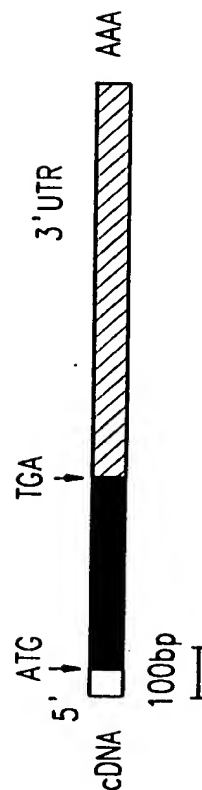FIG.1A

FIG.1B

FIGURE 2

```
1     CTTGAGAGGCTCTGGCTCTTGCTTCTTAGGCGGCCCGAGGACGCCATGGCCGAGTGCCCG
                                                        M  A  E  C  P
61    ACACTCGGGGAGGCAGTCACCGACCACCCGGACCGCCTGTGGGCCTGGGAGAAGTTCGTG
       T  L  G  E  A  V  T  D  H  P  D  R  L  W  A  W  E  K  F  V
121   TATTTGGACGAGAAGCAGCACGCCTGGCTGCCCTTAACCATCGAGATAAAGGATAGGTTA
       Y  L  D  E  K  Q  H  A  W  L  P  L  T  I  E  I  K  D  R  L
181   CAGTTACGGGTGCTCTTGCGTCGGGAAGACGTCGTCCTGGGGAGGCCTATGACCCCCACC
       Q  L  R  V  L  L  R  R  E  D  V  V  L  G  R  P  M  T  P  T
241   CAGATAGGCCCAAGCCTGCTGCCTATCATGTGGCAGCTCTACCCTGATGGACGATACCGA
       Q  I  G  P  S  L  L  P  I  M  W  Q  L  Y  P  D  G  R  Y  R
301   TCCTCAGACTCCAGTTTCTGGCGCTTAGTGTACCACATCAAGATTGACGGCGTGGAGGAC
       S  S  D  S  S  F  W  R  L  V  Y  H  I  K  I  D  G  V  E  D
361   ATGCTTCTCGAGCTGCTGCCAGATGACTGATGTATGGTCTTGGCAGCACCTGTCTCCTTT
       M  L  L  E  L  L  P  D  D  *  114
421   CACCCCAGGGCCTGAGCCTGGCCAGCCTACAATGGGGATGTTGTGTTTCTGTTCACCTTC
481   GTTTACTATGCCTGTGTCTTCTCCACCACGCTGGGGTCTGGGAGGAATGGACAGACAGAG
541   GATGAGCTCTACCCAGGGCCTGCAGGACCTGCCTGTAGCCCACTCTGCTCGCCTTAGCAC
601   TACCACTCCTGCCAAGGAGGATTCCATTTGGCAGAGCTTCTTCCAGGTGCCCAGCTATAC
661   CTGTGCCTCGGCTTTTCTCAGCTGGATGATGGTCTTCAGCCTCTTTCTGTCCCTTCTGTC
721   CCTCACAGCACTAGTATTTCATGTTGCACACCCACTCAGCTCCGTGAACTTGTGAGAACA
781   CAGCCGATTCACCTGAGCAGGACCTCTGAAACCCTGGACCAGTGGTCTCACATGGTGCTA
841   CGCCTGCATGTAAACACGCCTGCAAACGCTGCCTGCCGGTAAACACGCCTGCAAACGCTG
901   CCTGCCCGTAAACACGCCTGCAAACGCTGCCTGCCCACACAGGTTCACGTGCAGCTCAAG
961   GAAAGGCCTGAAAGGAGCCCTTATCTGTGCTCAGGACTCAGAAGCCTCTGGGTCAGTGGT
1021  CCACATCCCGGGACGCAGCAGGAGGCCAGGCCGGCGAGCCCTGTGGATGAGCCCTCAGAA
1081  CCCTTGGCTTGCCCACGTGGAAAAGGGATAGAGGTTGGGTTTCCCCCCTTTATAGATGGT
1141  CACGCACCTGGGTGTTACAAAGTTGTATGTGGCATGAATACTTTTTGTAATGATTGATTA
1201  AATGCAAGATAGTTTATCTAACTTCGTGCGCAATCAGCTTCTATCCTTGACTTAGATTCT
1261  GGTGGAGAGAAGTGAGAATAGGCAGCCCCCAAATAAAAAATATTCATGGAAAAAAAAAAA
1321  AAAA  1324
```
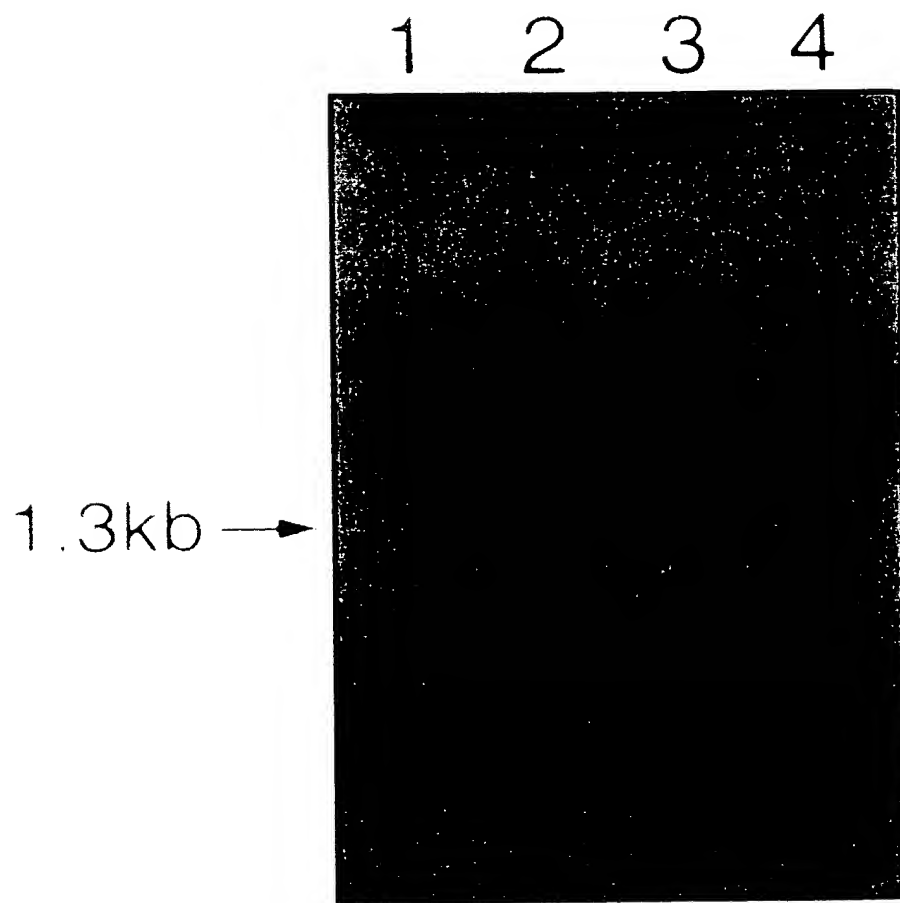
FIG.3A

```
1     GTCGACTGTGAGTTCCCAGCAGAGGCCCAGAGTCCCGGTCCGGCAGCCGAGGGAAGCGGG
61    GGGGTCTTCCAGAAGAAGAAAGGGCCAAGGTCACCCCGGTGCCTCTCCAGCAGCAGCAGA
121   GGGCGGCGGTCGGTGTCGCTGCTGGCCGGGGCCTCGAGGAAGGCGCGGGCCAGCTGGGGC
181   CGGGTCTGCCGTTCCCAGGAGCTGCCACCGTTCCAGGGAGCAAGTCAGGCCGGGACGTTAG
241   CGCCTGCGCGGGACCCTCACTTGCCACCAAGGACCCCACAAACCCCGCCCCATCCTTAGC
301   GCCTGCGCGGGACCCTCACTTGCCACCAAGACCCCCACAAACCCCGCCCCATCCTGCCTT
361   ACGCCCCGCCCCAAGGTCGTTCTCCCGACCCGGGGTCCCGCCCCAAGACCGTCCTCCCGC
421   CCCGCCGCTTGGTGGCGGCCCGCATGCTGCCCCGGATATAAAGGGTCGGCCCCACATCCCAG
481   GGACCAGCGAGCGGCCTTGAGAGGCTCTGGCTCTTGCTTCTTAGGCGGCCCGAGGACGCC
541   ATGGCCGAGTGCCCGACACT  560
```

FIG.3B

1   2   3
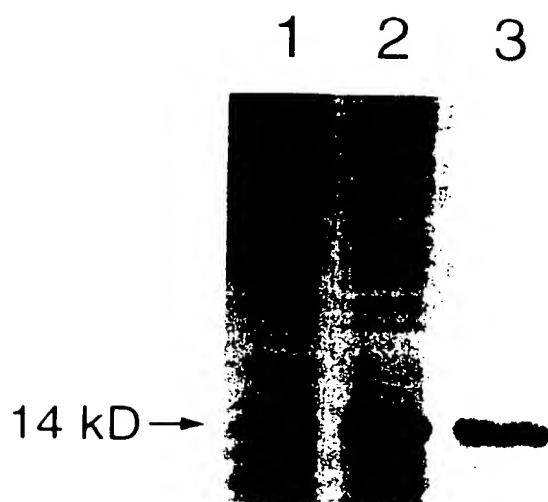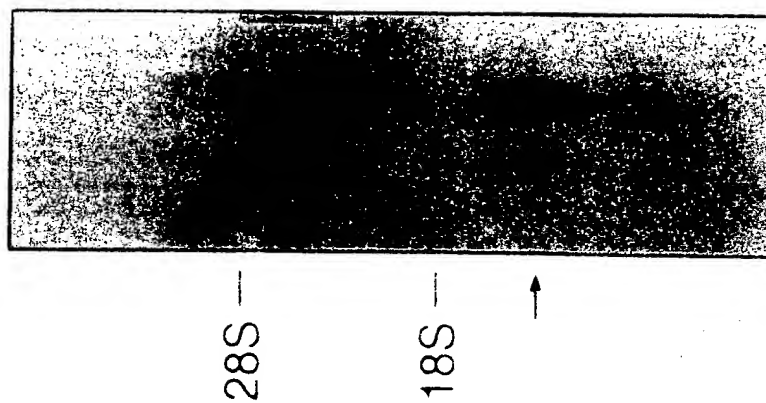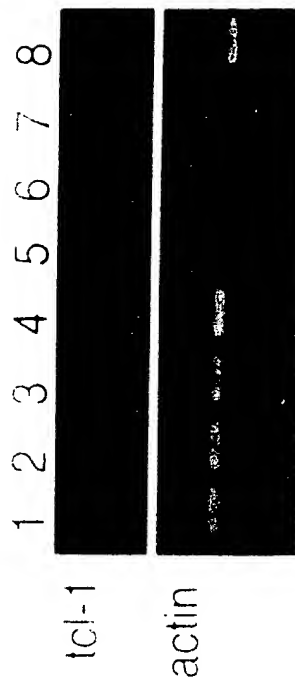
14 kD→

FIG.4

FIGURE 5B

FIGURE 5C

FIGURE 5A

1 2 3 4 5 6

1.3 Kb →

1 2 3 4 5 6 7 8

tcl-1

actin

PBL
PBL + PHA
SUPT11

28S —

18S —

FIGURE 6

1 2 3 4 5 6

Tcl-1 →

1 2 3 4 5 6

Actin →
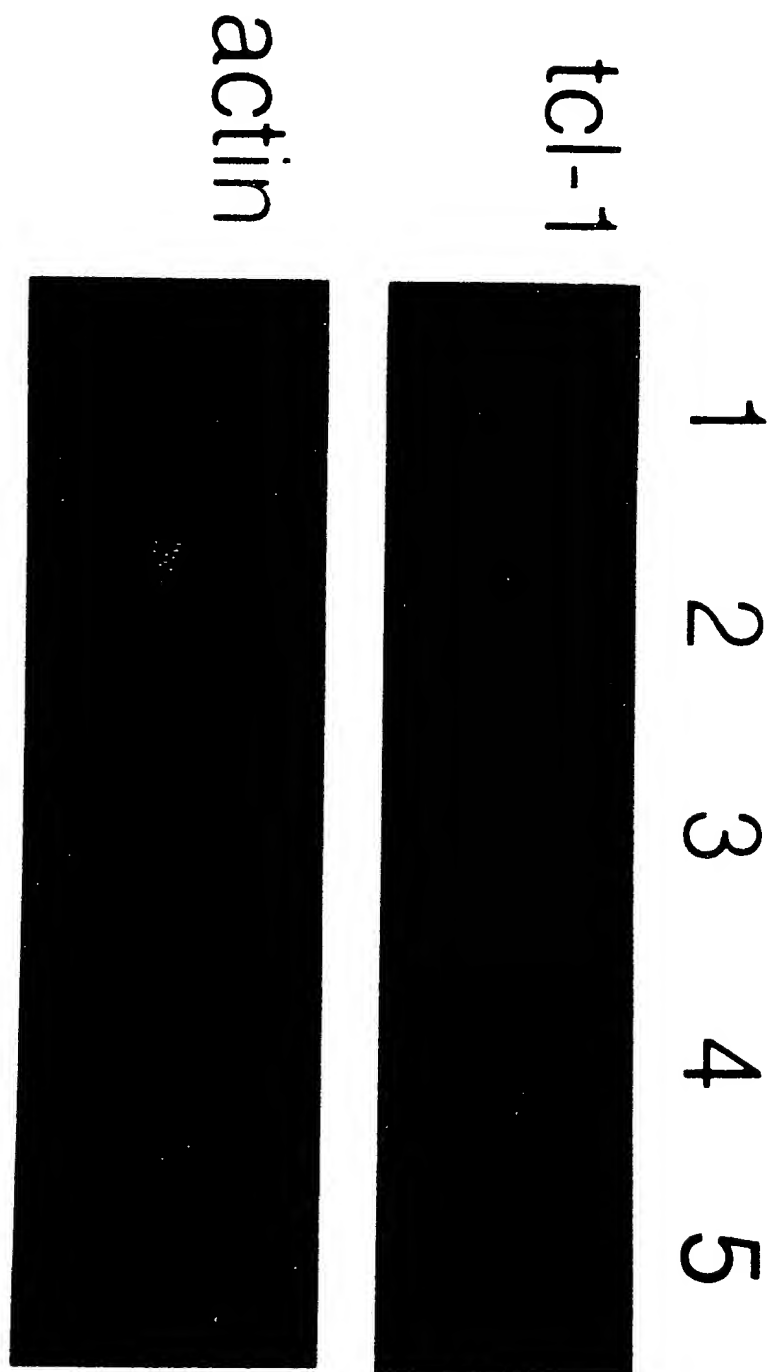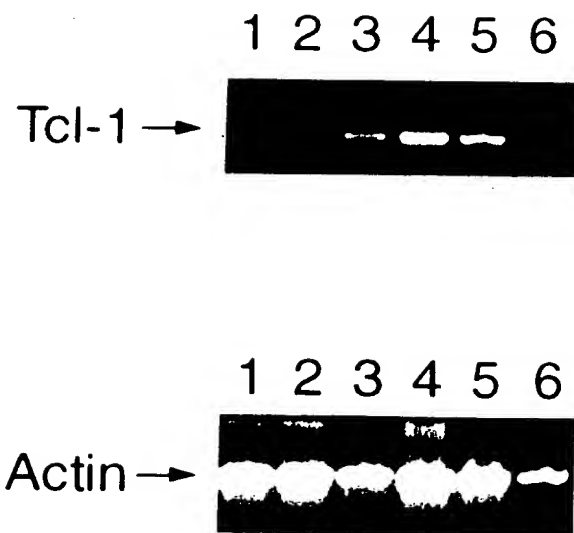
FIG.7

```
                    10        20        30        40        50        60
TCL-1   MAECPTLGEAVTDHPDRLWAWEKFVYLDEKQHAWLPLTIEIKDRLQLRVLLRREDVVLGR
             | |::|:|: :: || ||| ::|::: :| :::|| :|| : ::: :| ||
MTCP1   MAGEDVGAPPDHLWVHQEGIYRDEYQRTWVAV-VEEETSF-LRARVQQIQVPLGD
                    10        20        30        40        50

                    70        80        90       100       110
TCL-1   SMTPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDDX
        : |::: :| ||||||:| |:::|::::: :|::: || :|::|||||||
MTCP1   AARPSHLLTSQLPLMWQLYPEERYMDNNSRLWQIQHHLMVRGVQELLKLLPDDX
                    60        70        80        90       100
```

FIG.8

```
   1   GTCGACTTGT GAKTYCCMAG MAGAGGCCCA GAAGTCCCGGTCCGGCAAAG

  51   CGGAGGGGAA GCGGGGGGGG TCTTCCAAGA AGAAGAAAGGGCCCAAGGTT

 101   CAACCCCCGG TGCCTTCTCC AGCAGCAAGC AAGAGGGCGGCGGGTCGGTT

 151   GTCGCTGCTG GCCGGGGCCC TCCGAGGAAA GGCGCGGRCCAGCTGGGGCC

 201   GGGTCTGCGT TCCCAGGAGC TGCCACCGTT CCAGGGAGCAAGTCAGGCCG

 251   GGACGTTAGC GCCTGCGCGG GACCCTCACT TGCCACCAAGRMCCCCACAA

 301   ACCCCGCCCC ATCCTGYCTT ACGCCCCGCC CCAAGGTCGGTTCTCCCCGA

 351   CCCGGGGGTC CCGCCCCCAA GGNCCGTCCT CCCCGCCCCCGCCGSTTGGT

 401   GGCGGCCGCA TGCTGCCCGG ATATAAAGGG TCGGCCCCACATCCCAGGGA

 451   CCAGCGAGCG GCCTTGAGAG GCTCTGGCTC TTGCTTCTTAGGCGGCCCGA

 501   GGACGCCATG GCCGAGTGCC CGACACTCGG GGAGGCAGTCACCGACCACC

 551   CGGACCGCCT GTGGGCCTGG GAGAAGTTCG TGTATTTGGACGAGAAGCAG

 601   MACGCCTGCC TGCCCTTAAC CATCGAGGTA CAACCACCTTTGGAGCGGAT

 651   GGCGARGCAG CAGGGGCASC CCCTGGGAGC TTGGGATNCCCTAGGAAGGG

 701   CGAGGACTCA AGGAGCACTC ACTATGGGGC AGGGAGGATCCCCCACAGAT

 751   KAAGCCACTT TTGGAGCCGG SCTCTKGAGG GATGAATAGGAGTTCCTCCA

 801   GGCAGGGAAG AAGGGTGGGA AAACCCCAAA GGAATGTCGGTCAAAGGGGT

 851   GGACCCAGTG CCTGTGGAGT GTGACTATAA TGTTGACTACAGCAGGCATT

 901   TTCTGGGCTT CGGGGTCCTA ATCCTTAAAA ATGGGTATCTCTAAGTGACT

 951   CATCCATATG GCCGATTATC GGAATCATCT CAGGTGGGTCCCAGAAATCT

1001   GTATTTTTAA AAAGAACCCW CMACAGTTTA GGGTCCAACCCAGGCATAAC

1051   CAAAACACTG GCCTAAGAGT TGTGAAGTAT TTTCCCACCTACCCTCTGGG

1101   CTTTATTTAA GAMAACCAAA TTTAACAAGT GATGTCGTAGTATAAGCGCC

1151   GGTANTKGAA YCAATATTGA CTTTTTTAAT GTGTGATGCCTTAAGATGGG

1201   TCCTTAATCC ATGTTAAGNT TTTGTTAAAG AAATAGATAAGTCTTTTACA

1251   AGTATTTGGA TTTACTCAAT GAAAAGAGT CANAAAATGTTCAAACTCTC

1301   TCCAAACATA CACTGAAGAA AGCATAAAAA TTANNAAATATATTAGAACA
```

FIGURE 9A

```
1351  CGTATGTCCA  GTAGCAAWCA  MAAATTATTG  AGTGTTGAYTGTGTCTCTAC

1401  AGATGGGAAA  CTGAGGCACA  CMAAATGTAC  ATTTGTCCGAGGTAAGATTG

1451  CTAGTAGGTA  ATGGGGTTGG  AATTCTAGGC  TCTTAACCACCACAAAATCT

1501  GCATTTTTAT  TGGCATTTCA  ATTTTTTAAA  TATGTTTTTACTTTAAAAAT

1551  CAAGTTAAAT  ACTTACTTTT  TTAAAATCAA  AATTTGAAGAAATAATTTGA

1601  AGATTCAGTG  GATTTCTTTT  TTTAAATCTC  TGAGAAATCTCTTCCCTYCA

1651  ACGTGACACC  MAAACCMGCG  AACCAGACAG  TTTTTCATAAAATCATGAAA

1701  CATGCYCCMC  MAAAAATAAC  CCACTASCAA  ACTGTGGGACAGATTTTGCC

1751  TCACATCATT  GAAAAGGCCA  GCAWTCTTTT  TCTCTCTTTCTTTCTTTGKT

1801  GTTTTTTTTT  TTTCCTGTAG  AWACAGGGTC  TCGCTCTGTGACCCAGGCTG

1851  GTCTYAAACT  CCTGGCCTCA  AGCGATCCTC  CTGCCTCTGCCTTCCAAAGC

1901  ACTGGAATTA  CAAGTGTGAG  CCGCTGCAAC  CCGCCAGAAAAAAGTGTGCC

1951  TTTCATGGCC  CTGTCTGGGT  GGCTAGACAC  GTGTGTGTGCTGGTGGTCCT

2001  GGCCCAGCCA  GAGTTCCCTG  AGAGGAGCAT  GCATGGCCTAAGGAAGTGAG

2051  CTTCAGGGAA  CAGTGATGAC  CATCATTTCA  CACTCGGACCCCCTGCCMAA

2101  GATGGGTGGA  TGSCTGSCAG  GGAGGGATTC  CGGTKTTCCTGCGCCTGGAG

2151  AANCCCTGCC  AAGCGGAACC  TGAAAGTATN  CCCTGTCCTTTTCTTCTCCT

2201  NAGATAAAGG  ATAGGTTACA  GTTNNGGGTG  CTCTTGCGTCGGGAAGACGT

2251  CGTCCTGGGG  AGGCCTATGA  CCCCCACCNA  GATAGGCCCAAGCCTGCTGC

2301  CTATCATGTG  GCAGCTCTAC  CCTGATGGAC  GATACCGATCCTCAGACTCC

2351  AGTTTCTGGC  GCTTAGTGTA  CCACATCAAG  GTGAGTGTCTTTCTCCCAGA

2401  GGTCCATCGG  KTGATCTTGG  GTTTCCCCTC  CYCMATGTCTGSCCTTAGTG

2451  GTTTAYCTTC  CCYCCATCCC  AGTSSGCAAA  AGCATTWAAAARATGGGGGA

2501  NRTRWACMAS  TGCAGATTTC  TANAGGACTT  TACCAGAGAGAAGANAGATC

2551  CTNTGAGGTC  TCTAANAGAA  CCCTACCTCC  ACTTCCTCCCANCCACCANC

2601  TAACCGCAGG  AAGACATCTC  TGGTGGGGMM  KCACAGGCTGAAGGCTGGTG

2651  GGAGGAGGGR  CAKTCTCCAA  GASCCCCTGA  AATCCTCACACCTGGGTTCC
```

FIGURE 9B

```
2701  TACCTGCTGT TTCCAGCTAG GGGAAGSCSC AGGAGTGAGGAATGGAGGGA

2751  GTGGAGGGCT CTGGCCGATC AATGCCTTCT CTCTCTCTGCCTCTCAGA

2801  TTGACGGCGT GGAGGACATG CTTCTCGAGC TGCTGCCAGATGACTGATGT

2851  ATGGTGAGCT CCACTGGAGC CTGACCCCTC TTAGTCCACAGTGGCTGTAT

2901  CAGAAAGAAA GACCACCCCT TCTCCATGAA GGCAGTGCTAACCCCTCCCC

2951  GACTGCTGCC ATCTGAGGGT CCCTAGGGAT GGGAGAGGCTTCCTGGAGGC

3001  ACTCATGTCT CCCTTACCAC TTCGGGAGCC AAGGGCTTTGGTAGGCAGCC

3051  CCCTTTATCG CAGCTGCTCA TATCTATAAA GTACTTCACAAGTTTCAGCT

3101  GGCACTTTCA TTTTACCATT GCTTTTTTTT TCTTTGGGAGATGAGTCTGG

3151  CTCTGTGGCC CAGGCTAGAG TGTAGTGGGT GCAATCTCAGCTCACTGAAA

3201  GCTCTGCCTC CCGGGTTCAC ACCATTCTCC TGCCTCAGCCCTCGGAGTAG

3251  CTGGGACTAC AGGCGCCCGC CACCACACCT GGCTAATTTTTTTTTTTTTW

3301  TTWTWTTTTT TAGTAGAGMC GGGGTTTCAC CGTGTTAGCCAGGATGGTCT

3351  CGATCTCCTG ACCTCATGAT CTGCCCGCCT CGGCCTCCCAAAGTGCTGGG

3401  ATTACAGGCA TGAGCCACCA CGTCCGGCCT TACCATTGCTTTATTAAATA

3451  AGCACTGGTG CTTGATTATA TCAGCTGAGC CAGATATTAGATACGCTATT

3501  GAGTTTTGRG GAAATAAGAG TACCAAAACT CAGAAATGAGTTGAAGTATA

3551  GTGACATCTT CAGATTACAG ACCCAGGTGT CAGAATTTGCCTTGGCTCAG

3601  AAGGCCTCTG GGGGCCATCC CTGACCACTA GGCTTCCCACTTAGACCTGC

3651  TCCAGCAGCA CCACCCCTCG SCACTGCCTG GTCCTTTCCTTCACCCTTGA

3701  TTCTGTCTTC TTTTGTCCTT CTCCAGGTCT TGGYAGCACCTGTCTCCTTT

3751  CACCCCAGGG CCTGAGCCTG GCCAGCCTAC AATGGGGATGTTGTGTTTCT

3801  GTTCACCTTC GTTTACTATG BCTGTGTCTT CTCCACCACGCTGGGGTCTG

3851  GGAGGAATGG ACAGACAGAG GATGAGCTCT ACCCRGGGCCTGSAGGACCT

3901  GTCCTGTAGM CCACTCTGCT CGCCTTAGSA CCTACSACTCCWRCCGASGA

3951  GGATNCCANT TGGAAGAGCT TCTTNNAGGT GNCNAANAANANCTGTGCGT

4001  NGGCTTTTCT CAGCTGGATG ATGGTCNTNA GCCTCTTTCTGTCCCTTCTG
```

FIGURE 9C

```
4051   TCCCTCACAG CACTAGTATT TNATGTTGCA CACCCACTCAGCTCCGTGAA

4101   TTTGTGAGAA CACAACCGAT TCACCTGAGC AGGACCTCTGAAACCCTGGA

4151   CCAGTGGTCT CACATGGTGC TACGCCTGCA TGTAAACACGCCTNCAAACG

4201   CTGCCTGCCK GTRAACACGM SKSYRMACAG STGMSWRCCCGTAAACACGC

4251   CTGCAAACGC TGCCTGCCCA CACAGGTTCA CGTGCAGCTCAAGGAAAGRM

4301   CTGAAARRAG CCCTTATCTG TGCTCAGGAC TCAGAAGCCTCTGGGTCAGT

4351   GGTCCACATC CCGGGACGCA GNAGGAGGCC AGGCCGGCGAGCCCTGTGGA

4401   TGAGCCCTCA GAACCCTTGG GTTGCCCACG TGGAAAAGGGATAGAGGTTG

4451   GGTTTCCCCC CTTTTATAGA TGGTCACGCA CCTGGGTGTTACAAAGTTGT

4501   ATGTGGCATG AATACTTGNT GTNATGATTG ATTAAATGCAAGATAGTTTA

4551   TCTAACTTCG TGCGGAATCA GCTTCTATCC TTGNCTTAGATTCTGGTGGA

4601   GAGAAGTGAN AATAGGCAGN CCCCANATAA ANAATATTCANGGGATTTAT

4651   TTTATTNTTC CTTTTGGGNG ATNNGGGACT ACATTNTNCNNCCCCGTNTA

4701   ATCCAATGNT TAAANCCCCA GTGTTCTTGG AGGNCNTACGTCGAANACCA

4751   TTGGNGTANG CAACCTCAAA ATTTTTNNGT TGNNAATTNCCNGTTTTCCA

4801   GAGNCCCCCC CNTNCTCCAT CTTNNTCCTN GCCCNCCCTNNCCTCCCNCA

4851   NTCCCNANGT TNCCCTCGNC CCCAGTCAGT TCTTTCTCCNNCTTTANCCG

4901   NTNATNTCAC CAGNTTCTTT CT
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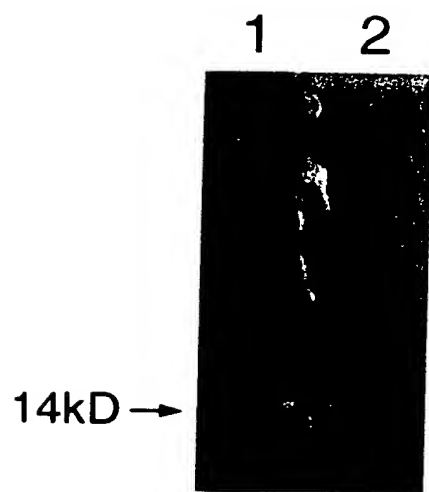
FIGURE 9D

FIG.10

FIG.11